RAW SEQUENCE LISTING

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Application Serial Number: 10630555

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(1) GENERAL INFORMATION: (i) APPLICANT: MIYAZONO, Kohei TEN DIJKE, Peter FRANZEN, Petra YAMASHITA, Hidetoshi HELDIN, Carl-Henrik (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS HAVING SERINE THREONINE KINASE DOMAINS, AND THEIR USE (iii) NUMBER OF SEQUENCES: 48 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Fulbright & Jaworski L.L.P. (B) STREET: 666 Fifth Avenue (C) CITY: New York City (D) STATE: New York (E) COUNTRY: USA (F) ZIP: 10103 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb (B) COMPUTER: IBM PS/2 (C) OPERATING SYSTEM: PC-DOS (D) SOFTWARE: Wordperfect (vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US/09/903,068C (B) FILING DATE: 11-Jul-2001 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: PCT/GB93/02367 (B) FILING DATE: November 17, 1993 (A) APPLICATION NUMBER: GB 9224057.1 (B) FILING DATE: November 17, 1992 (A) APPLICATION NUMBER: GB 9304677.9 (B) FILING DATE: March 8, 1993 (A) APPLICATION NUMBER: GB 9304680.3 (B) FILING DATE: March 8, 1993 (A) APPLICATION NUMBER: 9311047.6 (B) FILING DATE: May 28, 1993 (A) APPLICATION NUMBER: 9313763.6 (B) FILING DATE: July 2, 1993 (A) APPLICATION NUMBER: 9316099.2 (B) FILING DATE: August 3, 1993 (A) APPLICATION NUMBER: 321344.5 (B) FILING DATE: October 15, 1993 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Norman D. Hanson (B) REGISTRATION NUMBER: 30,946 (C) REFERENCE/DOCKET NUMBER: LUD 5298.4 DIV (10105901) (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (212) 318-3000 (B) TELEFAX: (212) 318-3400 (2) INFORMATION FOR SEQ ID NO: 1: (i) SEOUENCE CHARACTERISTICS: (A) LENGTH: 1984 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(A) NAME/KEY: CDS (B) LOCATION: 283..1791 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC 294 Met Thr Leu Gly TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG 342 Ser Pro Arg Lys Gly Leu Leu Met Leu Met Ala Leu Val Thr Gln GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT 390 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA 438 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC 486 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC 534 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC 582 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser 95 CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT 630 Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG 678 Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu 125 GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG 726 Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Gln Glu 140 AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG 774 Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT 822 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser

170

GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG

175

(ix) FEATURE:

870																
	Asp	Cys	Thr	Thr	Gly 185	Ser	Gly	Ser	Gly	Leu 190	Pro	Phe	Leu	Val	Gln 195	Arg
918	ACA	GTG	GCA	CGG	CAG	GTT	GCC	TTG	GTG	GAG	TGT	GTG	GGA	AAA	GGC	CGC
710	Thr	Val	Ala	Arg 200	Gln	Val	Ala	Leu	Val 205	Glu	Cys	Val	Gly	Lys 210	Gly	Arg
966	TAT	GGC	GAA	GTG	TGG	CGG	GGC	TTG		CAC	GGT	GAG	AGT		GCC	GTC
	Tyr	Gly		Val	Trp	Arg	Gly		Trp	His	Gly	Glu		Val	Ala	Val
1014	AAG	ATC	215 TTC	TCC	TCG	AGG	GAT	GAA	CAG	TCC	TGG	TTC	225 CGG	GAG	ACT	GAG
1014	Lys		Phe	Ser	Ser	Arg		Glu	Gln	Ser	Trp		Arg	Glu	Thr	Glu
1000	ATC	230 TAT	AAC	ACA	GTA	TTG	235 CTC	AGA	CAC	GAC	AAC	240 ATC	CTA	GGC	TTC	ATC
1062		Tyr	Asn	Thr	Val		Leu	Arg	His	Asp		Ile	Leu	Gly	Phe	
	245 GCC	TCA	GAC	ATG	ACC	250 TCC	CGC	AAC	TCG	AGC	255 ACG	CAG	CTG	TGG	CTC	260 ATC
1110	Ala	Ser	Asp	Met		Ser	Arg	Asn	Ser		Thr	Gln	Leu	Trp		Ile
	ACG	CAC	TAC	CAC	265 GAG	CAC	GGC	TCC	CTC	270 TAC	GAC	TTT	CTG	CAG	275 AGA	CAG
1158	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu		Arg	Gln
	ACG	CTG	GAG	280 CCC	CAT	CTG	GCT	CTG	285 AGG	СТА	GCT	GTG	TCC	290 GCG	GCA	TGC
1206	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	Ala	Ala	Cys
	GGC	CTG	295 GCG	CAC	CTG	CAC	GTG	300 GAG	ATC	TTC	GGT	ACA	305 CAG	GGC	AAA	CCA
1254	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro
	GCC	310 ATT	GCC	CAC	CGC	GAC	315 TTC	AAG	AGC	CGC	AAT	320 GTG	CTG	GTC	AAG	AGC
1302	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	Leu	Val	Lys	Ser
	325			TGT		330					335					340
1350				Cys												
				GAT	345					350					355	
1398				Asp					•							
		_		360 ATG	_		_		365					370		
1446				Met												
	_	_	375	TCC				380		_			385			
1494				Ser												
	_	390		ATT	_		395					400				
1542																
	405	_		Ile		410					415					420
1590	TAT	AGA	CCA	CCC	TTC	TAT	GAT	GIG	GIG	CCC	AAT	GAC		AGC	1 1 T	UAU

	Tyr	Arg	Pro	Pro		Tyr	Asp	Val	Val		Asn	Asp	Pro	Ser	Phe	Glu
	GAC	ATG	AAG	AAG	425 GTG	GTG	TGT	GTG	GAT	430 CAG	CAG	ACC	CCC	ACC		CCT
1638	Asp	Met	Lys	_	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	Pro	Thr 450	Ile	Pro
1686	AAC	CGG	CTG	440 GCT	GCA	GAC	CCG	GTC		TCA	GGC	CTA	GCT		ATG	ATG
	Asn	Arg	Leu 455	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu	Ala 465	Gln	Met	Met
1734	CGG	GAG		TGG	TAC	CCA	AAC		TCT	GCC	CGA	CTC	ACC	GCG	CTG	CGG
	Arg	Glu 470	Cys	Trp	Tyr	Pro	Asn 475	Pro	Ser	Ala	Arg	Leu 480	Thr	Ala	Leu	Arg
1782	ATC		AAG	ACA	CTA	CAA		ATT	AGC	AAC	AGT		GAG	AAG	CCT	AAA
1702	Ile 485	Lys	Lys	Thr	Leu	Gln 490	Lys	Ile	Ser	Asn	Ser 495	Pro	Glu	Lys	Pro	Lys 500
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC																
	Val Ile Gln TGGGGGGGTG GGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG															
1891																
1951																
1984																
,	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 503 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear															
	(ii) MOLECULE TYPE: protein(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala															
	1			_	5		_	_	_	10					15	
				20	-	-			25			_	Gly	30		
	Thr	Cys	Thr 35	Cys	Glu	Ser	Pro	His 40	Cys	Lys	Gly	Pro	Thr 45	Cys	Arg	Gly
	Ala	Trp 50	Cys	Thr	Val	Val	Leu 55	Val	Arg	Glu	Glu	Gly 60	Arg	His	Pro	Gln
	Glu 65	His	Arg	Gly	Cys	Gly 70	Asn	Leu	His	Arg	Glu 75	Leu	Cys	Arg	Gly	Arg 80
					85			_	_	90	_		His		95	
	His	Asn	Val	Ser 100	Leu	Val	Leu	Glu	Ala 105	Thr	Gln	Pro	Pro	Ser 110	Glu	Gln
	Pro	Gly	Thr 115	Asp	Gly	Gln	Leu	Ala 120	Leu	Ile	Leu	Gly	Pro 125	Val	Leu	Ala
	Leu	Leu 130	Ala	Leu	Val	Ala	Leu 135	Gly	Val	Leu	Gly	Leu 140	Trp	His	Val	Arg
	Arg 145	Arg	Gln	Glu	Lys	Gln 150	Arg	Gly	Leu	His	Ser 155	Glu	Leu	Gly	Glu	Ser 160
	Ser	Leu	Ile	Leu	Lys 165	Ala	Ser	Glu	Gln	Gly 170	Asp	Thr	Met	Leu	Gly 175	Asp
	Leu	Leu	Asp	Ser 180		Cys	Thr	Thr	Gly 185	-	Gly	Ser	Gly	Leu 190	Pro	Phe
	T.eu	Val	Gln		Thr	Val	Ala	Arq		Val	Ala	Leu	Val	Glu	Cys	Val

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Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
                       215
                                            220
Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
                                      235
                  230
Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
                                  250
               245
Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
                               265
Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
                           280
Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
                       295
                                           300
Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
                   310
                                       315
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
                                    330
Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
                               345
Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
                           360
Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
                      375
Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
                                       395
                   390
Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
                                    410
Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
                                425
Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
                            440
Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
                        455
Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
                   470
                                        475
Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
                                    490
Glu Lys Pro Lys Val Ile Gln
           500
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(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
 - (-) FRICKER STREET
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:

115

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..1630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG

60 GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA

Met Val Asp Gly